

SEQUENCE LISTING

<110> Munger, Karl and Syken, Josh

<120> Methods and Reagents to Regulate Apoptosis

<130> HMV-054.01

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 2656

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (32) .. (1474)

<400> 1

gaattcgcgg ccgcagagtc cccggggccaa g atg gct gcg cgg tgc tcc aca 52

Met Ala Ala Arg Cys Ser Thr

1

5

cgc tgg ttg ctg gtg gtt gtg ggg acc ccg cgg ctg ccg gct ata tcg 100

Arg Trp Leu Leu Val Val Val Gly Thr Pro Arg Leu Pro Ala Ile Ser

10

15

20

ggc aga ggg gcc cgg ccg ccc agg gag ggc gtg gtg ggg gca tgg ctg 148

Gly Arg Gly Ala Arg Pro Pro Arg Glu Gly Val Val Gly Ala Trp Leu

25

30

35

agc cgc aag ctg agc gtc ccc gcc ttt gcg tct tcc ctg acc tct tgc 196

Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys

40

45

50

55

ggc ccc cga gcg ctg ctg aca ttg aga cct ggt gtc agc ctt aca gga 244

Gly Pro Arg Ala Leu Leu Thr Leu Arg Pro Gly Val Ser Leu Thr Gly

60

65

70

aca aaa cat aac cct ttc att tgt act gcc tcc ttc cac acg agt gcc 292

Thr Lys His Asn Pro Phe Ile Cys Thr Ala Ser Phe His Thr Ser Ala

75

80

85

cct ttg gcc aaa gaa gat tat tat cag ata tta gga gtg cct cga aat 340

Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu Gly Val Pro Arg Asn

90

95

100

gcc agc cag aaa gag atc aag aaa gcc tat tat cag ctt gcc aag aag 388

Ala Ser Gln Lys Glu Ile Lys Lys Ala Tyr Tyr Gln Leu Ala Lys Lys

105

110

115

tat cac cct gac aca aat aag gat gat ccc aaa gcc aag gag aag ttc 436

Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys Ala Lys Glu Lys Phe

120

125

130

135

tcc cag ctg gca gaa gcc tat gag gtt ttg agt gat gag gtg aag agg 484

Ser Gln Leu Ala Glu Ala Tyr Glu Val Leu Ser Asp Glu Val Lys Arg

140	145	150	
aag cag tac gat gcc tac ggc tct gca ggc ttc gat cct ggg gcc agc Lys Gln Tyr Asp Ala Tyr Gly Ser Ala Gly Phe Asp Pro Gly Ala Ser 155 160 165			532
ggc tcc cag cat agc tac tgg aag gga ggc ccc act gtg gac ccc gag Gly Ser Gln His Ser Tyr Trp Lys Gly Gly Pro Thr Val Asp Pro Glu 170 175 180			580
gag ctg ttc agg aag atc ttt ggc gag ttc tca tcc tct tca ttt gga Glu Leu Phe Arg Lys Ile Phe Gly Glu Phe Ser Ser Ser Ser Phe Gly 185 190 195			628
gat ttc cag acc gtg ttt gat cag cct cag gaa tac ttc atg gag ttg Asp Phe Gln Thr Val Phe Asp Gln Pro Gln Glu Tyr Phe Met Glu Leu 200 205 210 215			676
aca ttc aat caa gct gca aag ggg gtc aac aag gag ttc acc gtg aac Thr Phe Asn Gln Ala Ala Lys Gly Val Asn Lys Glu Phe Thr Val Asn 220 225 230			724
atc atg gac acg tgt gag cgc tgc aac ggc aag ggg aac gag ccc ggc Ile Met Asp Thr Cys Glu Arg Cys Asn Gly Lys Gly Asn Glu Pro Gly 235 240 245			772
acc aag gtg cag cat tgc cac tac tgt ggc ggc tcc ggc atg gaa acc Thr Lys Val Gln His Cys His Tyr Cys Gly Gly Ser Gly Met Glu Thr 250 255 260			820
atc aac aca ggc cct ttt gtg atg cgt tcc acg tgt agg aga tgt ggt Ile Asn Thr Gly Pro Phe Val Met Arg Ser Thr Cys Arg Arg Cys Gly 265 270 275			868
ggc cgc ggc tcc atc atc ata tgc ccc tgt gtg gtc tgc agg gga gca Gly Arg Gly Ser Ile Ile Ile Ser Pro Cys Val Val Cys Arg Gly Ala 280 285 290 295			916
gga caa gcc aag cag aaa aag cga gtg atg atc cct gtg cct gca gga Gly Gln Ala Lys Gln Lys Lys Arg Val Met Ile Pro Val Pro Ala Gly 300 305 310			964
gtc gag gat ggc cag acc gtg agg atg cct gtg gga aaa agg gaa att Val Glu Asp Gly Gln Thr Val Arg Met Pro Val Gly Lys Arg Glu Ile 315 320 325			1012
ttc att acg ttc agg gtg cag aaa agc cct gtg ttc cgg agg gac ggc Phe Ile Thr Phe Arg Val Gln Lys Ser Pro Val Phe Arg Arg Asp Gly 330 335 340			1060
gca gac atc cac tcc gac ctc ttt att tct ata gct cag gct ctt ctt Ala Asp Ile His Ser Asp Leu Phe Ile Ser Ile Ala Gln Ala Leu Leu 345 350 355			1108
ggg gga aca gcc aga gcc cag ggc ctg tac gag acg atc aac gtg acg Gly Gly Thr Ala Arg Ala Gln Gly Leu Tyr Glu Thr Ile Asn Val Thr 360 365 370 375			1156

atc ccc cct ggg act cag aca gac cag aag att cgg atg ggt ggg aaa	1204
Ile Pro Pro Gly Thr Gln Thr Asp Gln Lys Ile Arg Met Gly Gly Lys	
380 385 390	
ggc atc ccc cgg att aac agc tac ggc tac gga gac cac tac atc cac	1252
Gly Ile Pro Arg Ile Asn Ser Tyr Gly Tyr Gly Asp His Tyr Ile His	
395 400 405	
atc aag ata cga gtt cca aag agg cta acg agc cgg cag cag agc ctg	1300
Ile Lys Ile Arg Val Pro Lys Arg Leu Thr Ser Arg Gln Gln Ser Leu	
410 415 420	
atc ctg agc tac gcc gag gac gag aca gat gtg gag ggg acg gtg aac	1348
Ile Leu Ser Tyr Ala Glu Asp Glu Thr Asp Val Glu Gly Thr Val Asn	
425 430 435	
ggc gtc acc ctg acc agc tct ggt ggc agc acc atg gat agc tcc gca	1396
Gly Val Thr Leu Thr Ser Ser Gly Gly Ser Thr Met Asp Ser Ser Ala	
440 445 450 455	
gga agc aag gct agg cgt gag gct ggg gag gac gag gag gga ttc ctt	1444
Gly Ser Lys Ala Arg Arg Glu Ala Gly Glu Asp Glu Glu Gly Phe Leu	
460 465 470	
tcc aaa ctt aag aaa atg ttt acc tca tga tatccagcc gaggaaaaag	1494
Ser Lys Leu Lys Lys Met Phe Thr Ser	
475 480	
atccactgga aactaggccg ggaagcagca gccctccaa gggccagggc acctgggaga	1554
cgaggaggatt ccagaacagc agcactgagc tcccacccgc agagcctctg gacggccttg	1614
gcaacagcaa aatcatggga caacacctct ctccacggaa aggtcacagt ggacagcccg	1674
ggcagtagga tgcagcccca gaggtggtg gcagtttctt gtccattggt aggtgacggc	1734
cccctggtca gcagaggaga ggtagatct tgcaggctaa aactctaatt tggaattgaa	1794
tattgtggat atcttagtta aaggccatgc ttacagctta gaaatgaagc cttagctgc	1854
atcaagttac gaagtgatta atttcttct cagcaaacct ccgggagggt ccagaatgag	1914
tttttctga caggttgtct tctactgggag cgtggggccc ccaggcccca ccagcaccgt	1974
cctccccata tgagggggccc tgccgaggca tcagctgtc tgctcagtta gtttttattc	2034
ccgggggtacc aagcagctgc acagtcggtg cctgggaagc acgttaaagg ccagagaga	2094
tcctgggggt tctgctctga ccgtgtgggt ggtgatcctt gtcaggatgt acagtccttg	2154
ctccaccccc atccgggatg gccgcctgtc cctgactatt gagtctgtt gttgtaagcc	2214
aggcatggag ggctcctgcc cttctgctga gccacagccc attgcagcac tgtgctggcc	2274
agacttcagc tgccttgga actgaagccc tgccactgtt gctagtcagg ggcttggttc	2334

tcccacttac actggtgaca tctatcttct gaagtgtgtt taaattattc agtgctaatac 2394
attgtttttt cctttgtaaa tgttgattca gaaaaggaaa gcacaggcta agcagttgaa 2454
ggttccccac cattcagtga gagcagaacc cccattcccc agcctctgct ggtagcatgt 2514
cgcagtttcc atgtgtttca ggatcttcgg gctgtcgtta gacagggtta tgaagaacac 2574
ttctcaacag ttctcttttt gttttccttt ataattcact aaaataaagc atctattagt 2634
gtctgaaaaa aaaaaaaaaa aa 2656

<210> 12
<211> 480
<212> PRT
<213> homo sapiens
<400> 2

Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
1 5 10 15
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
20 25 30
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
35 40 45
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
50 55 60
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
65 70 75 80
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
85 90 95
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
100 105 110
Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
115 120 125
Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
130 135 140
Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
145 150 155 160

Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
 165 170 175

Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
 180 185 190

Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
 195 200 205

Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
 210 215 220

Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
 225 230 235 240

Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
 245 250 255

Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
 260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
 275 280 285

Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
 290 295 300

Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
 305 310 315 320

Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser
 325 330 335

Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile
 340 345 350

Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu
 355 360 365

Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln
 370 375 380

Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly
385 390 395 400

Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
405 410 415

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
420 425 430

Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly
435 440 445

Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly
450 455 460

Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser
465 470 475 480

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG GCT GCG CGG TGC TCC ACA CGC TGG TTG CTG GTG GTT GTG GGG ACC	48
Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr	
1 5 10 15	
CCG CGG CTG CCG GCT ATA TCG GGT AGA GGG GCC CGG CCG CCC AGG GAG	96
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu	
20 25 30	
GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe	
35 40 45	
GCG TCT TCC CTG ACC TCT TGC GGC CCC CGA GCG CTG CTG ACA TTG AGA	192
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg	
50 55 60	
CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr	
65 70 75 80	
GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
85 90 95	
ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
TAT TAT CAG CTT GCC AAG AAG TAT CAC CCT GAC ACA AAT AAG GAT GAT	384

Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	
	115						120					125				
CCC	AAA	GCC	AAG	GAG	AAG	TTC	TCC	CAG	CTG	GCA	GAA	GCC	TAT	GAG	GTT	432
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	
	130					135					140					
TTG	AGT	GAT	GAG	GTG	AAG	AGG	AAG	CAG	TAC	GAT	GCC	TAC	GGC	TCT	GCA	480
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	
145					150					155					160	
GGC	TTC	GAT	CCT	GGG	GCC	AGC	GGC	TCC	CAG	CAT	AGC	TAC	TGG	AAG	GGA	528
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
			165					170						175		
GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG	576
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
			180					185					190			
TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT	624
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	
			195				200					205				
CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC	672
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	
	210					215					220					
AAC	AAG	GAG	TTC	ACC	GTG	AAC	ATC	ATG	GAC	ACG	TGT	GAG	CGC	TGC	AAC	720
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
225					230					235					240	
GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT	768
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	
			245						250					255		
GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT	816
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	
			260					265					270			
TCC	ACG	TGT	AGG	AGA	TGT	GGT	GGC	CGC	GGC	TCC	ATC	ATC	ATA	TCG	CCC	864
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	
		275					280						285			
TGT	GTG	GTC	TGC	AGG	GGA	GCA	GGA	CAA	GCC	AAG	CAG	AAA	AAG	CGA	GTG	912
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	
	290					295					300					
ATG	ATC	CCT	GTG	CCT	GCA	GGA	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG	960
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	
305					310					315					320	
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	1008
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	
			325						330					335		
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	1056
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
			340					345					350			
TCT	ATA	GCT	CAG	GCT	CTT	CTT	GGG	GGA	ACA	GCC	AGA	GCC	CAG	GGC	CTG	1104
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	
		355					360						365			
TAC	GAG	ACG	ATC	AAC	GTG	ACG	ATC	CCC	CCT	GGG	ACT	CAG	ACA	GAC	CAG	1152
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	
	370					375					380					
AAG	ATT	CGG	ATG	GGT	GGG	AAA	GGC	ATC	CCC	CGG	ATT	AAC	AGC	TAC	GGC	1200
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	
	385				390					395					400	
TAC	GGA	GAC	CAC	TAC	ATC	CAC	ATC	AAG	ATA	CGA	GTT	CCA	AAG	AGG	CTA	1248
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu	
			405						410					415		
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA	1296

Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
			420					425					430				
GAT	GTG	GAG	GGG	ACG	GTG	AAC	GGC	GTC	ACC	CTC	ACC	AGC	TCT	GGT	GGC		1344
Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Gly		
		435					440					445					
AGC	ACC	ATG	GAT	AGC	TCC	GCA	GGA	AGC	AAG	GCT	AGG	CGT	GAG	GCT	GGG		1392
Ser	Thr	Met	Asp	Ser	Ser	Ala	Gly	Ser	Lys	Ala	Arg	Arg	Glu	Ala	Gly		
	450					455				460							
GAG	GAC	GAG	GAG	GGA	TTC	CTT	TCC	AAA	CTT	AAG	AAA	ATG	TTT	ACC	TCA		1440
Glu	Asp	Glu	Glu	Gly	Phe	Leu	Ser	Lys	Leu	Lys	Lys	Met	Phe	Thr	Ser		
465					470				475						480		
TGA																	

1443

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Ala	Arg	Cys	Ser	Thr	Arg	Trp	Leu	Leu	Val	Val	Val	Gly	Thr		
1				5					10					15			
Pro	Arg	Leu	Pro	Ala	Ile	Ser	Gly	Arg	Gly	Ala	Arg	Pro	Pro	Arg	Glu		
			20					25					30				
Gly	Val	Val	Gly	Ala	Trp	Leu	Ser	Arg	Lys	Leu	Ser	Val	Pro	Ala	Phe		
	35					40					45						
Ala	Ser	Ser	Leu	Thr	Ser	Cys	Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg		
	50					55				60							
Pro	Gly	Val	Ser	Leu	Thr	Gly	Thr	Lys	His	Asn	Pro	Phe	Ile	Cys	Thr		
	65				70				75					80			
Ala	Ser	Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln		
			85						90					95			
Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala		
			100					105					110				
Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp		
	115					120						125					
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val		
	130					135					140						
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala		
	145				150				155					160			
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly		
			165					170						175			
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu		
			180					185					190				
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro		
	195					200						205					
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val		
	210					215					220						
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn		
	225				230					235				240			
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys		
			245						250					255			
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg		
			260					265					270				
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro		
	275					280						285					
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val		

290	295	300
Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met		
305	310	315
Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser		
	325	330
Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile		
	340	345
Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu		
	355	360
Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln		
	370	375
Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly		
385	390	395
Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu		
	405	410
Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr		
	420	425
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly		
	435	440
Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly		
	450	455
Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser		
465	470	475
		480

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCT GCG CGG TGC TCC ACA CGC TGG TTG CTG GTG GTT GTG GGG ACC	48
Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr	
1 5 10 15	
CCG CGG CTG CCG GCT ATA TCG GGT AGA GGG GCC CCG CCG CCC AGG GAG	96
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu	
20 25 30	
GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe	
35 40 45	
GCG TCT TCC CTG ACC TCT TGC GGC CCC CGA GCG CTG CTG ACA TTG AGA	192
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg	
50 55 60	
CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr	
65 70 75 80	
GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
85 90 95	
ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
TAT TAT CAG CTT GCC AAG AAG TAT CAC CCT GAC ACA AAT AAG GAT GAT	384

Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	
	115						120					125				
CCC	AAA	GCC	AAG	GAG	AAG	TTC	TCC	CAG	CTG	GCA	GAA	GCC	TAT	GAG	GTT	432
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	
	130						135					140				
TTG	AGT	GAT	GAG	GTG	AAG	AGG	AAG	CAG	TAC	GAT	GCC	TAC	GGC	TCT	GCA	480
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	
	145					150					155				160	
GGC	TTC	GAT	CCT	GGG	GCC	AGC	GGC	TCC	CAG	CAT	AGC	TAC	TGG	AAG	GGA	528
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
				165					170					175		
GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG	576
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
			180						185				190			
TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT	624
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	
	195						200					205				
CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC	672
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	
	210					215					220					
AAC	AAG	GAG	TTC	ACC	GTG	AAC	ATC	ATG	GAC	ACG	TGT	GAG	CGC	TGC	AAC	720
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
	225				230					235					240	
GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT	768
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	
			245						250				255			
GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT	816
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	
			260					265				270				
TCC	ACG	TGT	AGG	AGA	TGT	GGT	GGC	CGC	GGC	TCC	ATC	ATC	ATA	TCG	CCC	864
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	
		275					280					285				
TGT	GTG	GTC	TGC	AGG	GGA	GCA	GGA	CAA	GCC	AAG	CAG	AAA	AAG	CGA	GTG	912
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	
	290					295					300					
ATG	ATC	CCT	GTG	CCT	GCA	GGA	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG	960
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	
	305				310					315					320	
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	1008
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	
			325						330				335			
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	1056
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
			340					345					350			
TCT	ATA	GCT	CAG	GCT	CTT	CTT	GGG	GGA	ACA	GCC	AGA	GCC	CAG	GGC	CTG	1104
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	
		355					360					365				
TAC	GAG	ACG	ATC	AAC	GTG	ACG	ATC	CCC	CCT	GGG	ACT	CAG	ACA	GAC	CAG	1152
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	
	370					375					380					
AAG	ATT	CGG	ATG	GGT	GGG	AAA	GGC	ATC	CCC	CGG	ATT	AAC	AGC	TAC	GGC	1200
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	
	385				390					395					400	
TAC	GGA	GAC	CAC	TAC	ATC	CAC	ATC	AAG	ATA	CGA	GTT	CCA	AAG	AGG	CTA	1248
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu	
			405						410					415		
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA	1296

Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr
 420 425 430
 GAT GTG GAG GGG ACG GTG AAC GGC GTC ACC CTC ACC AGC TCT GGA AAA 1344
 Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Lys
 435 440 445
 AGA TCC ACT GGA AAC TAG 1362
 Arg Ser Thr Gly Asn
 450

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Ala Arg Cys Ser Thr Arg Trp Leu Leu Val Val Val Gly Thr
 1 5 10 15
 Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu
 20 25 30
 Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe
 35 40 45
 Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
 50 55 60
 Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
 65 70 75 80
 Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
 85 90 95
 Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
 100 105 110
 Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
 115 120 125
 Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
 130 135 140
 Leu Ser Asp Glu Val Lys Arg Lys Gln Tyr Asp Ala Tyr Gly Ser Ala
 145 150 155 160
 Gly Phe Asp Pro Gly Ala Ser Gly Ser Gln His Ser Tyr Trp Lys Gly
 165 170 175
 Gly Pro Thr Val Asp Pro Glu Glu Leu Phe Arg Lys Ile Phe Gly Glu
 180 185 190
 Phe Ser Ser Ser Ser Phe Gly Asp Phe Gln Thr Val Phe Asp Gln Pro
 195 200 205
 Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
 210 215 220
 Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
 225 230 235 240
 Gly Lys Gly Asn Glu Pro Gly Thr Lys Val Gln His Cys His Tyr Cys
 245 250 255
 Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
 260 265 270
 Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
 275 280 285
 Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
 290 295 300
 Met Ile Pro Val Pro Ala Gly Val Glu Asp Gly Gln Thr Val Arg Met
 305 310 315 320
 Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser

				325					330					335			
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile		
			340					345					350				
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu		
		355					360					365					
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln		
	370					375					380						
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly		
385					390				395						400		
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu		
			405					410					415				
Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
		420						425				430					
Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Lys		
	435						440					445					
Arg	Ser	Thr	Gly	Asn													
	450																

20465107.1